

2025

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(iii) NUMBER OF SEQUENCES: 21

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(A) MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
(B) COMPUTER: Compatible PC IBM (80486, 8 M Ram).
(C) OPERATING SYSTEM: Windows 95.
(D) SOFTWARE: Word Perfect 5.0 for Windows 95.

(A) APPLICATION NUMBER: 08/930,917
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(C) CLASSIFICATION:

(A) APPLICATION NUMBER: PCT/CU97/00001
(B) FILING DATE: 17-Jan-1997

(A) NAME: HENRY A. MARZULLO, JR.
(B) REGISTRATION NUMBER: 20.910

1
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic
(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1573

(D) OTHER INFORMATION: Primer 5' for PCR amplification of the first 44 amino acids of the recombinant protein of Neisseria meningitidis P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
TTCCATGGTA GATAAAAGAA TGGCTTTAG

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1575

(D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTTCTAGATC CAAAGTAATC AGGGTATCG

29

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: Primer 2192

(D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 120 amino acids of the

recombinant protein of *Neisseria meningitidis* P64K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
GGCGGTTCTG CCGATTAAGG ATCCGA

26

000120-62621260

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Fragment amplified by PCR

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genomic
- (B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Fragment derived from the first 47 amino acids of the recombinant protein of Neisseria meningitidis P64K, containing a NcoI site at the position 3 to 8 and a XbaI site at the position 139 to 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTCCATGGTA GATAAAAGAA TGGCTTTAGT TGAATTGAAA GTGCCCGACA
TTGGCGGACA 60

CGAAAATGTA GATATTATCG CGGTTGAAGT AACGTGGGC GACACTATTG
CTGTGGACGA 120

TACCCTGATT ACTTTGGATC TAGAAA
146

(2) INFORMATION FOR SEQ. ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

[illegible]

Table 1. Mean values of the variables measured during the 60-min test

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

Table 1. Mean values of the variables measured during the 60-min test

[illegible][illegible][illegible][illegible][illegible][illegible][illegible]

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[illegible][illegible][illegible][illegible]

16

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) **FRAGMENT TYPE:** Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: LR150

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation LR150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ser Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 10:

(A) SEQUENCE CHARACTERISTICS:

(B) LENGTH: 15 Amino acid residues

(C) TYPE: Amino acid

(D) STRANDEDNESS: Unknown

(E) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) **FRAGMENT TYPE:** Internal fragment

[illegible]

THE

(2) INFORMATION FOR SEQ. ID NO: 14:

(D) TOPOLOGY: Unknown

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) **FRAGMENT TYPE:** Internal fragment

(C) INDIVIDUAL ISOLATE: IIIB

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation IIIB.

Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
1 5 10 15

[illegible]

(D) TOPOLOGY: Unknown.

(iii) **HYPOTHETICAL: Yes**

(iv) ANTI-SENSE: No

(v) **FRAGMENT TYPE:** Internal fragment

(A) ORGANISM: VIH-1

multiepitopic polypeptide (MEP) TAB13.

1 5 10 15

(D) TOPOLOGY: Unknown

(iii) **HYPOTHETICAL: Yes**

(iv) ANTI-SENSE: No

(v) **FRAGMENT TYPE:** Internal fragment

(vi) ORIGINAL SOURCE:

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1

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[illegible]

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB4.

000740-04000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ala Pro Thr Ser Ser Ser Thr Ala Gln Thr Gln Leu Gln Leu Glu
 1 5 10 15
 His Leu Leu Leu Asp Leu Gln Ile Phe Leu Ser Arg Gly Ile Arg Ile
 20 25 30
 Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly Gly Gly Ala Arg Gln
 35 40 45
 Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr Thr Thr Ala Gly Gly
 50 55 60
 Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala
 65 70 75 80
 Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His Ile Gly Pro Gly Arg
 85 90 95
 Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile Thr Met
 100 105 110
 Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly Gly Gly Ala Ser Ile
 115 120 125
 Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
 130 135 140

(2) INFORMATION FOR SEQ. ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB9.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile
 1 5 10 15

OTHER INFORMATION: Codifies for epitopes V3 linked by the spacer of SEQ ID
NO: 17: in the
MEP TAB 19.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTAGACTCG AGAGGCATTC GTATCGGCCC AGGTCGCGCA
ATTTAGCAA CAGCTGGCGG 60

TGGCGCACGT CAATCTACCC CTATTGGTTT AGGTCAGGCT
CTGTATACGA CTGCCGGCGG 120

TGGTGCGCGC AAAAGTATCA CCAAGGGTCC AGGCCGCGTC
ATTACGCCA CCGCGGGCGG 180

CGGTGCCCCGT AAGCGTATCC ACATTGGCCC AGGCCGTGCA
TTCTATACTA CAGCAGGTGG 240

TGGCGCACGT AAACGCATCA CTATGGGTCC TGGTCGCGTC
TATTACACGA CCGCTGGCGG 300

CGGTGCTAGC ATTCGCATCC AACCGGCCC TGGTCGTGCA
TTTGTGACCA TATGATAACG 360

CGGGATCC

368

CGGTGCTAGC

SEQUENCE LISTING

SEQUENCE IDENTIFICATION NO.: 1

SEQUENCE TYPE: amino acid

LENGTH: 47 amino acids

MOLECULE TYPE: protein fragment.

PROPERTIES: First 47 amino acids of the recombinant protein P64k of *N. meningitidis*.

MLDKRMALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLETD 44

SEQUENCE IDENTIFICATION NO.: 2

SEQUENCE TYPE: Nucleotide

LENGTH: 29 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 5' No. 1573 for PCR amplification of the first 44 amino acids from the P64k antigen of *N. meningitidis*.

TTCCATGGTAGATAAAAGAATGGCTTTAG 29

SEQUENCE IDENTIFICATION NO.: 3

SEQUENCE TYPE: Nucleotide

LENGTH: 29 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 3' No. 1575 for PCR amplification of the first 44 amino acids from the P64k antigen of *N. meningitidis*.

TTTCTAGATCCAAAGTAATCAGGGTATCG 29

SEQUENCE IDENTIFICATION NO.: 4

SEQUENCE TYPE: Nucleotide

LENGTH: 26 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 3' No. 2192 for PCR amplification of the first 120 amino acids from the P64k antigen of *N. meningitidis*.

GGCGGTTCTGCCGATTAAGGATCCGA 26

SEQUENCE IDENTIFICATION NO.: 5

SEQUENCE TYPE: Nucleotide

LENGTH: 146 base pairs

MOLECULE TYPE: PCR amplified fragment

PROPERTIES: Derived fragment from the first 47 amino acids of the P64k antigen of *N. meningitidis*. Restriction sites NcoI (positions 3 to 8) and XbaI (positions 139 to 144) are introduced by PCR, which provoke changes in the nucleotide sequence of this fragment.

TTCCATGGTAGATAAAAGAATGGCTTTAGTTGAATTGAAAGTGCCCGACATTGGCGGACA 60
CGAAAATGTAGATATTATCGCGGTTGAAGTAAACGTGGGCGACACTATTGCTGTGGACGA 120
TACCCTGATTACTTTGGATCTAGAAA 146

SEQUENCE IDENTIFICATION NO.: 6
SEQUENCE TYPE: amino acid
LENGTH: 47 amino acids
MOLECULE TYPE: stabiliser fragment derived from the first 47 amino acids of the P64k antigen of *N. meningitidis*.
PROPERTIES: This fragment has the following changes with respect to the P64k.
L2→V2; E45→D45; T46→L46; D47→E47

MVDKRMALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLDLE 47

SEQUENCE IDENTIFICATION NO.: 7
SEQUENCE TYPE: Nucleotide
LENGTH: 16 bases
MOLECULE TYPE: Synthetic oligonucleotide

CTAGATTTGATATCAG 16

SEQUENCE IDENTIFICATION NO.: 8
SEQUENCE TYPE: Nucleotide
LENGTH: 16 bases
MOLECULE TYPE: Synthetic oligonucleotide

GATCCTGATATCAAAT 16

SEQUENCE IDENTIFICATION NO.: 9
SEQUENCE TYPE: amino acid
LENGTH: 15 amino acids
MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1.
LR150 isolate.

SRGIRIGPGRILAT 15

15

15

5

TAGGGASIRIQRGPGRFVTI 141

MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB9.

MVDKRMALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLDLDSRGIRIGPGRail 60
ATAGGGARQSTPIGLGGALYTTAGGGARKSITKGPGRVIYATAGGGARKRIHIGPGRFY 120
TTAGGGARKRITMGPRVYYTTAGGGASIRIQRGPGRFVTI 162

SEQUENCE IDENTIFICATION NO.: 20
SEQUENCE TYPE: amino acid
LENGTH: 202 amino acids
MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB13.

MVDKRMALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLDLDSRGIRIGPGRail 60
ATAGGGAROSTPIGLGOALYTTAGGGARKSITKGPGRVIYATAGGGARKRIHIGPGRFY 120
TTAGGGARKRITMGPRVYYTTAGGGARORTSIGOGOALYTTAGGGATSITIGPGOVFYR 180
TGAGGGASIRIQRGPGRFVTI 202

SEQUENCE IDENTIFICATION NO.: 21
SEQUENCE TYPE: Nucleotide
LENGTH: 368 base pairs
MOLECULE TYPE: Synthetic oligonucleotide
PROPERTIES: Nucleotide fragment that codifies for the V3 epitopes bound by a AGGGA spacer in the MEP TAB9. Restriction sites XbaI (positions 1 to 6) and BamHI (positions 363 to 368) are introduced.

TCTAGACTCGAGAGGCATTTCGTATCGGCCAGGTCGCGCAATTTAGCAACAGCTGGCGG 60
TGGCGCACGTCAATCTACCCCTATTGGTTTAGGTCAGGCTCTGTATACGACTGCCGGCGG 120
TGGTGCGCGCAAAAGTATCACCAAGGGTCCAGGCCGCGTCATTTACGCCACCGCGGGCGG 180
CGGTGCCCCGTAAGCGTATCCACATTGGCCCAGGCCGTGCATTCTATACTACAGCAGGTGG 240
TGGCGCACGTAAACGCATCACTATGGGTCCTGGTCGCGTCTATTACACGACCGCTGGCGG 300
CGGTGCTAGCATTTCGCATCCAACGCGGCCCTGGTCGTGCATTTGTGACCATATGATAACG 360
CGGGATCC 368

000T40"325T950

(C) DOCKET NUMBER: P-13

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (914) 723-4300

(B) TELEFAX: (914) 723-4301

(C) E-MAIL: HMARZULLO@LSMAG.COM

(2) INFORMATION FOR SEQ. ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: First 47 amino acids of the recombinant protein of Neisseria meningitidis P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp

35 40 45

(2) INFORMATION FOR SEQ. ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

000120 0253100